



-1-

SEQUENCE LISTING

<110> Gray et al.

<120> MACROPHAGE DERIVED CHEMOKINE (MDC), MDC ANALOGS, MDC INHIBITOR SUBSTANCES, AND USES THEREOF

<130> 27866/34810

<140> 09/509,165

<141> 2000-06-12

<150> 09/067,447

<151> 1998-04-28

<150> 08/939,107

<151> 1997-09-26

<150> 08/660,542

<151> 1996-06-07

<150> 08/558,658

<151> 1995-11-16

<150> 08/479,620

<151> 1995-06-07

<160> 46

<170> PatentIn Ver. 2.0

<210> 1

<211> 2923

<212> DNA

<213> Homo sapiens - human MDC cDNA

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<221> CDS

<222> (20)..(298)

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<221> mat_peptide

<222> (92)..(298)

<400> 1

gagacataca ggacagagc atg gct cgc cta cag act gca ctc ctg gtt gtc 52
Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val

-20

-15

ctc gtc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tac 100
Leu Val Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr

-10

-5

1

ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac 148
Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr
5 10 15

cgt ctg ccc ctg cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc 196
Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser
20 25 30 35

tgc ccg agg cct ggc gtg gtg cta acc ttc agg gat aag gag atc 244
Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile
40 45 50

tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg 292
Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
55 60 65

agc caa tgaagagcct actctgatga ccgtggcctt ggctcctcca ggaaggctca 348
Ser Gln

ggagccctac ctccctgcca ttatacgatgc tccccgccag aagccgtgc caactcttg 408
cattccctga tctccatccc tgtggctgac acccttggtc acctccgtgc tgtcaactg 468
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tgcccatgaa cggggccctc aagcgtcctg ggatctcctt ctccctcctg tcctgtctt 2868
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<210> 2
<211> 93
<212> PRT
<213> Homo sapiens - human MDC

<400> 2
Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Ala
-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
-5 -1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

(Handwritten mark)
<210> 3
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer JHSP6

<400> 3
gacactatacg aatagggc 18

<210> 4
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer M13

<400> 4
gtaaaaacgac ggccagt 17

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer T3.1

<400> 5
aattaaccct cactaaaggg

20

<210> 6
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer T7.1

<400> 6
gtaatacgac tcactatagg gc

22

<210> 7
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-1F

<400> 7
tctatctaga ggccctacg gcgccaacat ggaag

35

<210> 8
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-2R

<400> 8
caccggatcc tcattggctc agcttattga gaa

33

<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-4R

<400> 9
aatggatcca cagcacggag gtgaccaag

29

<210> 10

<211> 31

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer 390-3R

<400> 10

agtcaagctt agggcactct gggatcgga c

31

<210> 11

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-FX2

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tatcgatcc tggatcccgcg tggccctac ggcccaaca tggaa

45

<210> 12

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer GEX5

<400> 12

gaaatccagc aagtatatacg ca

22

<210> 13

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-Pel

<400> 13

attgcgtatgg ccggcccccta cggcccaac atggaa

36

<210> 14

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390RcH

<400> 14

gaccaagctt gagacataca ggacagagca

30

<210> 15

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390RcX

<400> 15

tggatctaga agttggcaca ggcttctgg

29

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer DC03

<400> 16

cgtaaatata acgactcact

20

<210> 17

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
390mycRX

<400> 17

tggatctaga tcaattcaag tcctcctcgc tgatcagctt ctgctttgg ctcagcttat 60

tgagaat

67

<210> 18

<211> 99

<212> PRT

<213> Homo sapiens - Hu MCP-3

<400> 18

Met Lys Ala Ser Ala Ala Leu Leu Cys Leu Leu Leu Thr Ala Ala Ala
-20 -15 -10

Phe Ser Pro Gln Gly Leu Ala Gln Pro Val Gly Ile Asn Thr Ser Thr
-5 1 5

Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu
10 15 20 25

Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg Glu Ala Val
30 35 40

Ile Phe Lys Thr Lys Leu Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln
45 50 55

Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr
60 65 70

Pro Lys Leu
75

<210> 19

<211> 99

<212> PRT

<213> Homo sapiens - Hu MCP-1

<400> 19

Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr
-20 -15 -10

Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val
-5 1 5

Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu
10 15 20 25

Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
30 35 40

Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln
45 50 55

Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr
60 65 70

Pro Lys Thr
75

<210> 20

<211> 76

<212> PRT

<213> Homo sapiens - Hu MCP-2

<400> 20

Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn Val Ile
1 5 10 15

Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg Ile Thr
20 25 30

Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg Gly
35 40 45

Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser Met
50 55 60

Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro
65 70 75

P | <210> 21

<211> 91

<212> PRT

<213> Homo sapiens - RANTES

<400> 21

Met Lys Val Ser Ala Ala Ala Leu Ala Val Ile Leu Ile Ala Thr Ala
-20 -15 -10

Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro
-5 1 5

Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys
10 15 20 25

Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe
30 35 40

Val Thr Arg Lys Asn Arg Gln Val Cys Ala Asn Pro Glu Lys Lys Trp
45 50 55

Val Arg Glu Tyr Ile Asn Ser Leu Glu Met Ser
60 65

<210> 22

<211> 91

<212> PRT

<213> Homo sapiens - MIP-1 beta

<400> 22
Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
-20 -15 -10

Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr
-5 1 5

Ala Cys Cys Phe Ser Tyr Thr Arg Glu Ala Ser Ser Asn Phe Val Val
10 15 20 25

Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe
30 35 40

Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp
45 50 55

Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn
60 65

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<210> 23
<211> 92
<212> PRT
<213> Homo sapiens - MIP-1 alpha

<400> 23

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
-20 -15 -10

Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
-5 1 5 10

Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
15 20 25

Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
30 35 40

Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
45 50 55

Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
60 65 70

<210> 24
<211> 96
<212> PRT
<213> Homo sapiens - I-309

<400> 24
Met Gln Ile Ile Thr Thr Ala Leu Val Cys Leu Leu Leu Ala Gly Met
-20 -15 -10

Trp Pro Glu Asp Val Asp Ser Lys Ser Met Gln Val Pro Phe Ser Arg
-5 1 5 10

Cys Cys Phe Ser Phe Ala Glu Gln Glu Ile Pro Leu Arg Ala Ile Leu
15 20 25

Cys Tyr Arg Asn Thr Ser Ser Ile Cys. Ser Asn Glu Gly Leu Ile Phe
30 35 40

Lys Leu Lys Arg Gly Lys Glu Ala Cys Ala Leu Asp Thr Val Gly Trp
45 50 55

Val Gln Arg His Arg Lys Met Leu Arg His Cys Pro Ser Lys Arg Lys
60 65 70

<210> 25
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Human MDC Analog

<220>
<221> misc_feature
<222> (24)
<223> Xaa = arg, gly, ala, val, leu, ile,
pro, ser, thr, phe, tyr, trp, aspartate,
glutamate, asn, gln, cys, or met

<220>
<221> misc_feature
<222> (27)
<223> Xaa = lys, gly, ala, val, leu, ile, pro, ser, thr, phe, tyr, trp,
aspartate, glutamate, asn, gln, cys, or met

<220>
<221> misc_feature
<222> (30)
<223> Xaa = tyr, ser, lys, arg, his, aspartate, glutamate, asn, gln, or
cys

<220>
<221> misc_feature
<222> (50)
<223> Xaa = glu, lys, arg, his, gly, or ala

<220>
<221> misc_feature
<222> (59)
<223> Xaa = trp, ser, lys, arg, his, aspartate, glutamate, asn, gln, or cys

<220>
<221> misc_feature
<222> (60)
<223> Xaa = val, ser, lys, arg, his, aspartate, glutamate, asn, gln, or cys

<400> 25
Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Ala
-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
-5 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Xaa
10 15 20

Val Val Xaa His Phe Xaa Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Xaa Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Xaa Xaa Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-7F

<400> 26
tattggatcc gttctagctc cctgttctcc 30

<210> 27
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-8R

<400> 27

ccaagaattc ctgcagccac tttctggct c

31

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer ARA1

<400> 28

gcgactctc actgtttctc

20

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer ARA2

<400> 29

cacaggaaac agctatgacc

20

<210> 30

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human MDC analog

<400> 30

Leu Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp
1 5 10 15

Tyr Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp
20 25 30

Thr Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg
35 40 45

Asp Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile
50 55 60

Leu Asn Lys Leu Ser Gln

65 70

<210> 31
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Human MDC analog

<400> 31
Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr
1 5 10 15

Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr
20 25 30

Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp
35 40 45

Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Tyr Leu Lys Met Ile Leu
50 55 60

Asn Lys Leu Ser Gln
65

<210> 32
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Human MDC analog

<400> 32
Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr
1 5 10 15

Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys Glu Tyr Phe Tyr Thr
20 25 30

Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp
35 40 45

Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu
50 55 60

Asn Lys Leu Ser Gln
65

<210> 33

<211> 1677

<212> DNA

<213> Homo sapiens - human CCR4 cDNA

<220>

<221> CDS

<222> (183)..(1262)

<400> 33

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agaaaagcaa gctgcttctg gttggggcca gacctgcctt gaggagcctg tagagttaaa 180

aa atg aac ccc acg gat ata gca gat acc acc ctc gat gaa agc ata 227
Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile

1

5

10

15

tac agc aat tac tat ctg tat gaa agt atc ccc aag cct tgc acc aaa 275
Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys
20 25 30

gaa ggc atc aag gca ttt ggg gag ctc ttc ctg ccc cca ctg tat tcc 323
Glu Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser
35 40 45

ttg gtt ttt gta ttt ggt ctg ctt gga aat tct gtg gtg gtt ctg gtc 371
Leu Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val
50 55 60

ctg ttc aaa tac aag cgg ctc agg tcc atg act gat gtg tac ctg ctc 419
Leu Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu
65 70 75

aac ctt gcc atc tcg gat ctg ctc ttc gtg ttt tcc ctc cct ttt tgg 467
Asn Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp
80 85 90 95

ggc tac tat gca gca gac cag tgg gtt ttt ggg cta ggt ctg tgc aag 515
Gly Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys
100 105 110

atg att tcc tgg atg tac ttg gtg ggc ttt tac agt ggc ata ttc ttt 563
Met Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe
115 120 125

gtc atg ctc atg agc att gat aga tac ctg gcg ata gtg cac gcg gtg 611
Val Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val
130 135 140

ttt tcc ttg agg gca agg acc ttg act tat	ggg gtc atc acc agt	ttg	659
Phe Ser Leu Arg Ala Arg Thr	Leu Thr Tyr Gly Val Ile Thr Ser Leu		
145	150	155	
gct aca tgg tca gtg gct gtg ttc gcc tcc ctt	cct ggc ttt ctg ttc		707
Ala Thr Trp Ser Val Ala Val Phe Ala Ser	Leu Pro Gly Phe Leu Phe		
160	165	170	175
agc act tgt tat act gag cgc aac cat acc tac	tgc aaa acc aag tac		755
Ser Thr Cys Tyr Thr Glu Arg Asn His	Thr Tyr Cys Lys Thr Lys Tyr		
180	185	190	
tct ctc aac tcc acg acg tgg aag gtt ctc agc	tcc ctg gaa atc aac		803
Ser Leu Asn Ser Thr Thr Trp Lys Val Leu Ser	Ser Leu Glu Ile Asn		
195	200	205	
att ctc gga ttg gtg atc ccc tta ggg atc atg	ctg ttt tgc tac tcc		851
Ile Leu Gly Leu Val Ile Pro Leu Gly Ile Met	Leu Phe Cys Tyr Ser		
210	215	220	
atg atc atc agg acc ttg cag cat tgt aaa aat	gag aag aag aac aag		899
Met Ile Ile Arg Thr Leu Gln His Cys Lys Asn	Glu Lys Lys Asn Lys		
225	230	235	
gcg gtg aag atg atc ttt gcc gtg gtc ctc	ttc ctt ggg ttc tgg		947
Ala Val Lys Met Ile Phe Ala Val Val Val	Leu Phe Leu Gly Phe Trp		
240	245	250	255
aca cct tac aac ata gtg ctc ttc cta gag	acc ctg gtg gag cta gaa		995
Thr Pro Tyr Asn Ile Val Leu Phe Leu Glu	Thr Leu Val Glu Leu Glu		
260	265	270	
gtc ctt cag gac tgc acc ttt gaa aga tac	ttg gac tat gcc atc cag		1043
Val Leu Gln Asp Cys Thr Phe Glu Arg Tyr	Leu Asp Tyr Ala Ile Gln		
275	280	285	
gcc aca gaa act ctg gct ttt gtt cac tgc	tgc ctt aat ccc atc atc		1091
Ala Thr Glu Thr Leu Ala Phe Val His Cys	Cys Leu Asn Pro Ile Ile		
290	295	300	
tac ttt ttt ctg ggg gag aaa ttt cgc aag	tac atc cta cag ctc ttc		1139
Tyr Phe Phe Leu Gly Glu Lys Phe Arg Lys	Tyr Ile Leu Gln Leu Phe		
305	310	315	
aaa acc tgc agg ggc ctt ttt gtg ctc tgc	caa tac tgt ggg ctc ctc		1187
Lys Thr Cys Arg Gly Leu Phe Val Leu Cys	Gln Tyr Cys Gly Leu Leu		
320	325	330	335
caa att tac tct gct gac acc ccc agc tca	tct tac acg cag tcc acc		1235
Gln Ile Tyr Ser Ala Asp Thr Pro Ser Ser	Tyr Thr Gln Ser Thr		
340	345	350	

atg gat cat gat ctt cat gat gct ctg tagaaaaat gaaatggta	1282
Met Asp His Asp Leu His Asp Ala Leu	
355	360
aatgcagagt caatgaactt ttccacattc agagcttact ttaaaaattgg tatttttagg	1342
taagagatcc ctgagccagt gtcaggagga aggcttacac ccacagtgga aagacagctt	1402
ctcatcctgc aggcaagctt ttctctccca ctagacaagt ccagcctggc aagggttcac	1462
ctgggctgag gcataccttcc tcacaccagg ctgcctgca ggcatgagtc agtctgatga	1522
gaactctgag cagtgcgttga atgaagttgt agttaatatt gcaaggcaaa gactattccc	1582
ttctaacctg aactgatggg tttctccaga gggattgca gagtactggc tgatggagta	1642
aatcgctacc tttgctgtg gcaaattggc ccccg	1677

<210> 34

<211> 360

<212> PRT

<213> Homo sapiens - human CCR4

<400> 34

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr			
1	5	10	15

Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu			
20	25	30	

Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu			
35	40	45	

Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu			
50	55	60	

Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn			
65	70	75	80

Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly			
85	90	95	

Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met			
100	105	110	

Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val			
115	120	125	

Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe			
130	135	140	

Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
145 150 155 160

Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
165 170 175

Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
180 185 190

Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
195 200 205

Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
210 215 220

Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
225 230 235 240

Val Lys Met Ile Phe Ala Val Val Leu Phe Leu Gly Phe Trp Thr
245 250 255

Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
260 265 270

Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
275 280 285

Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
290 295 300

Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
305 310 315 320

Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
325 330 335

Ile Tyr Ser Ala Asp Thr Pro Ser Ser Tyr Thr Gln Ser Thr Met
340 345 350

Asp His Asp Leu His Asp Ala Leu
355 360

<210> 35
<211> 1784
<212> DNA
<213> murine MDC cDNA

<220>
<221> CDS
<222> (1) .. (276)

<220>
<221> mat_peptide
<222> (73)..(276)

<400> 35

atg tct aat ctg cgt gtc cca ctc ctg gtg gct ctc gtc ctt ctt gct 48
Met Ser Asn Leu Arg Val Pro Leu Leu Val Ala Leu Val Leu Ala
-20 -15 -10

gtg gca att cag acc tct gat gca ggt ccc tat ggt gcc aat gtg gaa 96
Val Ala Ile Gln Thr Ser Asp Ala Gly Pro Tyr Gly Ala Asn Val Glu
-5 1 5

gac agt atc tgc tgc cag gac tac atc cgt cac cct ctg cca tca cgt 144
Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His Pro Leu Pro Ser Arg
10 15 20

tta gtg aag gag ttc ttc tgg acc tca aaa tcc tgc cgc aag cct ggc 192
Leu Val Lys Glu Phe Phe Trp Thr Ser Lys Ser Cys Arg Lys Pro Gly
25 30 35 40

gtt gtt ttg ata acc gtc aag aac cga gat atc tgt gcc gat ccc agg 240
Val Val Leu Ile Thr Val Lys Asn Arg Asp Ile Cys Ala Asp Pro Arg
45 50 55

cag gtc tgg gtg aag aag cta ctc cat aaa ctg tcc tagggaggag 286
Gln Val Trp Val Lys Lys Leu Leu His Lys Leu Ser
60 65

AA
gacctgatga ccatgggtct ggtgtggtcc agggaggctc agcaagccct attcttctgc 346

cattccagca agagccttgc caacgacgcc acctttactc acctccatcc cctgggctgt 406

cactctgtca ggctctggtc cctctacctc ccctctatcc cttccagctt atcccccttc 466

aatgtggcag ctgggaaaca cattcaggcc agccttaccc aatgcctact ccccactgct 526

ttagatgaga ccagcgctct tgtttgatg ccctgatcct atgatgcctt ccccatcccc 586

agccttggcc cccttctctt cttgcattgtc gggaggccc ataggtttca aatatgtct 646

acctaattcc ctttctgggg ggttctaata cccagcatgt tttcctgtct gcaggcacct 706

atccagtgcc acacacctcc caagtttcta tcagtccttccag tgggcattca ccaagccca 766

aacttcagac ttccttggcc tccacctact ctcagtagaa ttctggagttcaggctgg 826

tccaccaggc cccccagggt taggccaagg tccccaccag agtcctcctt gtttcttgg 886

ctgcagcactc gggcagggag caaggagcag gctcagaatc agatttctta aaggagctgc 946

agactccatc agtaaaaagga atctttctcc catccctgaa tataaggcag ttttctgtca 1006

acacagagac tcagggttggc agaaaatggcc acatagatca actgtgaaac cctaaattta 1066
ccaagaatca acttccaccc ctcttcaacc acatgctagg gtctttact ttctctgcc 1126
cacaccttg actccttgcc tggtagctg atagtcgaag ttatgctatg gtgtcagtga 1186
ctgccacagt ttgttggta ttataagcta tagttatatt tatataggaa agaggataaa 1246
tatatgtggg ccaaataagac gaactggaga gttttaggat ctggggcag gaaggccat 1306
acaaagtat acctcagaaa atagatggtt gtgggagctg ctgcaggatgg cagatgttac 1366
ttaaagaact taattgaaat tattcttgag tggctgaggc caagacaaga atatagaacc 1426
cattcttgct tccctggaga caacagtggt cccaggggaa ggaataaaacc ttcttgctcc 1486
tctggaggga gcatggcctg rcttagccga gtgactggac tgtgtgagat tgggggcatc 1546
gctttcccty tctgagccctc agctgacagc atatggacc acaaaggct tgatccaaac 1606
cacagggatt gacagtgcac gccacagctg tgtccagggc tcgtgttctg ccagaaggag 1666
cacctggacg accagggcca ccactagtgc tactttgctc actgcccattg catgtcctga 1726
aggccccctcc ccctccctcctc ctacttctgg gaaaataaat gctcgccaaat aatacctg 1784

AI
<210> 36
<211> 92
<212> PRT
<213> murine MDC

<400> 36

Met Ser Asn Leu Arg Val Pro Leu Leu Val Ala Leu Val Leu Leu Ala
-20 -15 -10

Val Ala Ile Gln Thr Ser Asp Ala Gly Pro Tyr Gly Ala Asn Val Glu
-5 1 5

Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His Pro Leu Pro Ser Arg
10 15 20

Leu Val Lys Glu Phe Phe Trp Thr Ser Lys Ser Cys Arg Lys Pro Gly
25 30 35 40

Val Val Leu Ile Thr Val Lys Asn Arg Asp Ile Cys Ala Asp Pro Arg
45 50 55

Gln Val Trp Val Lys Lys Leu Leu His Lys Leu Ser
60 65

<210> 37
<211> 958
<212> DNA
<213> rat MDC cDNA

<220>
<221> CDS
<222> (1) .. (243)

<220>
<221> mat_peptide
<222> (40) .. (243)

<220>
<221> misc_feature
<222> (206)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (785)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (827)
<223> n = A or G or T or C

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<220>
<221> misc_feature
<222> (836)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (861)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (864)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (871)
<223> n = A or G or T or C

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<221> misc_feature
<222> (878)
<223> n = A or G or T or C

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<221> misc_feature
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<223> n = A or G or T or C

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<223> n = A or G or T or C

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<223> n = A or G or T or C

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<223> n = A or G or T or C

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<222> (206)
<223> n = A or G or T or C

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<221> misc_feature
<222> (907)
<223> n = A or G or T or C

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<221> misc_feature
<222> (206)
<223> n = A or G or T or C

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<221> misc_feature
<222> (916)
<223> n = A or G or T or C

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<221> misc_feature
<222> (921)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (951)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (958)
<223> n = A or G or T or C

<400> 37

ctc gtc ctt ctt gct gtg gca ctt cag acc tcc gat gca ggt ccc tat 48
Leu Val Leu Leu Ala Val Ala Leu Gln Thr Ser Asp Ala Gly Pro Tyr
-10 -5 1

ggt gcc aat gtg gaa gac agt atc tgc tgc cag gac tac atc cgt cac 96
Gly Ala Asn Val Glu Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His
5 10 15

cct ctg cca cca cgt ttc gtg aag gag ttc tac tgg acc tca aag tcc 144
Pro Leu Pro Pro Arg Phe Val Lys Glu Phe Tyr Trp Thr Ser Lys Ser
20 25 30 35

tgc cgc aag cct ggc gtc gtt ttg ata acc atc aag aac cga gat atc 192
Cys Arg Lys Pro Gly Val Val Leu Ile Thr Ile Lys Asn Arg Asp Ile
40 45 50

tgt gct gac ccc ang atg ctc tgg gtg aag aag ata ctc cac aag ttg 240
Cys Ala Asp Pro Xaa Met Leu Trp Val Lys Lys Ile Leu His Lys Leu
55 60 65

gcc tagggagaag ggcctgatga ccacgggtct ggtgtctcca caaggctcag 293
Ala

caaaccctat cttctgcca tccagcaaga gccttgccaa caactccacc tttgctcacc 353

tccatcccct gggttgtcac tctgtgaagc ctgggtcccc tgtacttcct gtccgtcccc 413

tccagctcat tctcttccaa cgtggcagcc gggaaagcact tctggcttagc cttacccaat 473

actactcccc actgctttaa atgagaccag ggtccttgtt ttgggtgcctt tggatcctat 533

gatgccttcc cagtctccag cttggccccc cttctttct tacatgttagg gaacaccaat 593

atctttcaag tatgtgctac ccaattcctc ttccctggag gctgctggga cccggaatat 653

tatccccctgc tgcaggcctc tccaaggcacc actcacctcc caggcttcc atccgtcccc 713

gtcccaagcc ccatgcttca gaactccct tgccccccctt ctacactcca caaattctgg 773

ggaagtctca cnaactgggt cccctcaggc ccccacggga aggaaggccc cccnccaaca 833

acntcctcct gtttcccccg gtctcccncc nccgggantt gggcncccna atccccaaattt 893

tctgaanang aacngccccat tcttccctt aaaattaacc tttccccccc tccctgangt 953

taggn 958

<210> 38

<211> 81

<212> PRT

<213> rat

<220>

<221> misc_feature

<222> (56)

<223> Xaa = any or unknown amino acid

<400> 38

Leu Val Leu Leu Ala Val Ala Leu Gln Thr Ser Asp Ala Gly Pro Tyr
-10 -5 1

Gly Ala Asn Val Glu Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His
5 10 15

Pro Leu Pro Pro Arg Phe Val Lys Glu Phe Tyr Trp Thr Ser Lys Ser
20 25 30 35

Cys Arg Lys Pro Gly Val Val Leu Ile Thr Ile Lys Asn Arg Asp Ile
40 45 50

Cys Ala Asp Pro Xaa Met Leu Trp Val Lys Lys Ile Leu His Lys Leu
55 60 65

Ala

OR
<210> 39

<211> 506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: S. cerevisiae alpha factor pre-pro/human MDC cDNA chimeric construct

<220>

<221> CDS

<222> (15) .. (476)

<220>

<221> mat_peptide

<222> (270) .. (476)

<400> 39

atctcgagct cacg atg aga ttt cct tca att ttt act gca gtt tta ttc 50
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe
-85 -80 -75

gca gca tcc tcc gca tta gct gct cca gtc aac act aca aca gaa gat Ala Ala Ser Ser Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp	98	
-70	-65	-60
gaa acg gca caa att ccg gct gaa gct gtc atc ggt tac tta gat tta Glu Thr Ala Gln Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu	146	
-55	-50	-45
gaa ggg gat ttc gat gtt gct gtt ttg cca ttt tcc aac agc aca aat Glu Gly Asp Phe Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn	194	
-40	-35	-30
aac ggg tta ttg ttt ata aat act act att gcc agc att gct gct aaa Asn Gly Leu Leu Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys	242	
-25	-20	-15
-10		
gaa gaa ggg gta cct ttg gat aaa aga ggc ccc tac ggc gcc aac atg Glu Glu Gly Val Pro Leu Asp Lys Arg Gly Pro Tyr Gly Ala Asn Met	290	
-5	1	5
gaa gac agc gtc tgc cgt gat tac gtc cgt tac cgt ctg ccc ctg Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu	338	
10	15	20
cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc tgc ccg agg cct Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro	386	
25	30	35
ggc gtg gtg ttg cta acc ttc agg gat aag gag atc tgt gcc gat ccc Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro	434	
40	45	50
55		
aga gtg ccc tgg gtg aag atg att ctc aat aag ctg agc caa Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln	476	
60	65	
tgaaggcctt ctagagcggc cgcatcgata	506	

<210> 40
<211> 154
<212> PRT
<213> cDNA

<400> 40
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
-85 -80 -75 -70

Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln
-65 -60 -55

Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu Glu Gly Asp Phe
-50 -45 -40

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
-35 -30 -25

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
-20 -15 -10

Pro Leu Asp Lys Arg Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val
-5 1 5 10

Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys
15 20 25

His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu
30 35 40

Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp
45 50 55

Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 41

<211> 93

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human MDC Analog

J (<220>

<221> misc_feature

<222> (2)

<223> Xaa = not proline

<400> 41

Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Ala
-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Xaa Tyr Gly Ala Asn Met Glu
-5 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 42
<211> 538
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (53)..(334)

<220>
<221> mat_peptide
<222> (122)..(334)

<400> 42
ccctgagcag agggacctgc acacagagac tccctcctgg gtcctggca cc atg gcc 58
Met Ala

cca ctg aag atg ctg gcc ctg gtc acc ctc ctc ctg ggg gct tct ctg 106
Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Gly Ala Ser Leu
-20 -15 -10

cag cac atc cac gca gct cga ggg acc aat gtg ggc cgg gag tgc tgc 154
Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys
-5 1 5 10

ctg gag tac ttc aag gga gcc att ccc ctt aga aag ctg aag acg tgg 202
Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Thr Trp
15 20 25

tac cag aca tct gag gac tgc tcc agg gat gcc atc gtt ttt gta act 250
Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr
30 35 40

gtg cag ggc agg gcc atc tgt tcg gac ccc aac aac aag aag gtg aag 298
Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys
45 50 55

aat gca gtt aaa tac ctg caa agc ctt gag agg tct tgaaggctcc 344
Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
60 65 70

tcaccccaaga ctcctgactg tctccggga ctacctggga cctccaccgt tggtgttac 404
cgccccccacc ctgagcgcct gggtccaggg gaggccttcc agggacgaag aagagccaca 464

gtgagggaga tcccatcccc ttgtctgaac tggagccatg ggcacaaagg gcccagatta 524
aagtctttat cctc 538

<210> 43
<211> 94
<212> PRT
<213> Homo sapiens

<400> 43
Met Ala Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Gly Ala
-20 -15 -10

Ser Leu Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu
-5 1 5

Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys
10 15 20 25

Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe
30 35 40

Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg
45 50 55

Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
60 65 70

<210> 44
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
atgggaccat atggagcaaa tatggaagat agt 33

<210> 45
<211> 335
<212> DNA
<213> Macaque MDC

<220>
<221> CDS
<222> (19) . . (297)

<400> 45

agacatacag gacagagc atg gct cgc cta cag act gtg ttc ctg ggt gtc 51
Met Ala Arg Leu Gln Thr Val Phe Leu Gly Val
-20 -15

ctc atc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tat 99
Leu Ile Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr
-10 -5 1

ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac 147
Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr
5 10 15

cgt atg ccc ctg cgt gtg aaa cac ttc tac tgg acc tca gac tcc 195
Arg Met Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser
20 25 30 35

tgc ccg agg cct ggc gtg gtg ttg cta acc tcc agg gat aag gag atc 243
Cys Pro Arg Pro Gly Val Val Leu Leu Thr Ser Arg Asp Lys Glu Ile
40 45 50

tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg 291
Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
55 60 65

agc caa tgaagagcct actatgatga ccgtggccta agcaagcc 335
Ser Gln

<210> 46

<211> 93

<212> PRT

<213> Macaque MDC

<400> 46

Met Ala Arg Leu Gln Thr Val Phe Leu Gly Val Leu Ile Leu Leu Ala
1 5 10 15

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
20 25 30

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Met Pro Leu Arg
35 40 45

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
50 55 60

Val Val Leu Leu Thr Ser Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
65 70 75 80

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
85 90